zic5 gene. We have generated in situ probes that are specific for the *zic1*, *zic2*, *zic3*, and *zic4* genes in chick. While there is considerable overlap in the expression patterns of these genes, there are also distinct differences. *zic2* and *zic3* are strongly expressed in the entire dorsal neural tube, including the brain, trunk, and tail tip. *zic1* expression is strong in the dorsal brain, but weaker in the dorsal neural tube of the trunk. *zic4* appears to be expressed exclusively in the head region. During somite development, *zic1* is expressed dorsomedially in epithelial somites, while *zic2* expression begins well after somites have given rise to distinct dermomyotome and sclerotome regions. *zic1–3* are expressed strongly in the dorsomedial parts of more mature somites, particularly in the posterior portions. *zic2* is the only family member expressed in the periotic mesoderm in the hindbrain. *zic2–4* are expressed in the developing eye and all *zic* genes are expressed in the optic stalk. Among the *zic* genes, only *zic2* is expressed in the limb buds. We are currently analyzing *zic3* and *zic4* expression in more detail.

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Program/Abstract # 172
A microarray screen for direct targets of the Zic1 transcription factor

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The transcription factor zic1 plays important roles in a variety of developmental processes. In vertebrates, these include patterning the early neural plate, development of the neural crest, somite development, and formation of the cerebellum. In addition, zic1 promotes cell proliferation. To increase our understanding of the molecular mechanisms that underlie these processes, we have conducted a DNA microarray screen with Affymetrix gene chips to identify downstream target genes of zic1. The screen was performed using *Xenopus* ectodermal explants. By using an inducible zic1 construct (zic1GR) and the protein synthesis inhibitor cycloheximide, the screen was designed to discover direct targets of the Zic1 transcription factor. One new gene that was identified in this screen is the putative protease Xfeb that contributes to hindbrain patterning. We give a general overview of the genes identified in this screen and will discuss our findings from the screen with respect to genes involved in neural crest development and in anterior–posterior patterning.

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Program/Abstract # 173
Requirement of *Goosecoid* in early *Xenopus* development: A loss-of-function study

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Goosecoid (*Gsc*), a homeobox gene, was the first gene found to be specifically expressed in Spemann's organizer. In the present study, we show that knock-down of *Gsc* in *Xenopus* by Morpholino oligomers (MO) leads to loss of head structures and expansion of ventral tissues. Unlike in the mouse, our results demonstrate a requirement of *Gsc* for head formation and axis patterning in early *Xenopus* development. In search of downstream mediator genes, we found that the effects of *Gsc* completely depend on the BMP antagonist Chordin. Ectopic expression of mouse Gsc mRNA lead to induction of a secondary axis. Co-injection of Chordin MO prevented this inductive capability of Gsc mRNA in 97% of the embryos. Evidence for regulation of Chordin by Gsc is further provided by quantitative PCR and in situ hybridization, showing that Gsc MO decreases *Chordin* expression in gastrulating embryos. Moreover, loss-of-function experiments in animal cap explants revealed mutual repression of Gsc and the ventral homeobox transcription factors Vent1 and Vent2. MO-mediated knock-down of Vent1/2 caused strong dorsalization of the embryos, which could be suppressed by Gsc MO. Our results suggest that Gsc and Vent1/2 have opposing activities during gastrulation and act as regulators of each other in mesoderm patterning.

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Program/Abstract # 174
TFIIH trafficking and its nuclear assembly during early Drosophila embryo development

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We present the analysis of the dynamic of the transcription factor IIH (TFIIH) during early *Drosophila* embryo development. TFIIH consists of ten sub-units: cyclin-dependent kinase 7 (Cdk7), cyclin H and MAT1 (CAK), two helicases Xpb/Hay and Xpd, and p34, p44, p52, p42, p62 and p8 (core). We found that the TFIIH core is initially located in the cytoplasm of syncytial blastoderm embryos, after the mitotic division 10 and until the cellular blastoderm the core moves from the cytoplasm to the nucleus. The CAK complex has a different behaviour in early embryonic stages. The CAK is mostly cytoplasmic during cellularization and even during gastrulation. However, both components are positioned at promoters of genes that are activated at the onset of transcription. Later in development, the CAK complex becomes mostly nuclear and co-localizes in most chromosomal regions with the TFIIH core, but not in all sites, suggesting that the CAK complex could have a role in transcription of some loci without interaction with the TFIIH core. We also demonstrate that the CAK and the core coexist in the early embryo cytoplasm, however they do not interact until they are in the nucleus. Our data suggests that the complete assemble of the ten sub-units TFIIH occurs during the activation of zygotic transcription. In addition, we demonstrate that the